QR74.M65
Adams

STIC-ILL

From: Portner, Ginny
Sent: Monday, November 03, 2003 9:40 AM
To: STIC-ILL
Subject: 09/214,759

Importanc : High

10605582 96423170 PMID: 8825771
A physical and genetic map of Neisseria meningitidis B1940.
Gaher M; Einsiedler K; Crass T; Bautsch W
Institut fur Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Germany.
Molecular microbiology (ENGLAND) Jan 1996, 19 (2) p249-59, ISSN 0950-382X Journal Code: 8712028
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

STIC-ILL

Vol 10

470524

From: Portner, Ginny
Sent: Monday, November 03, 2003 10:03 AM
T : STIC-ILL
Subject: 09/214759

Importance: High

1865494 75040396 PMID: 4214776
Studies on gonococcus infection. V. Observations on in vitro interactions of gonococci and human neutróphils.
Swanson J ; Sparks E; Zeligs B; Siam M A; Parrott C
Infection and immunity (UNITED STATES) Sep 1974 , 10 (3) p633-44, ISSN 0019-9567 Journal Code: 0246127
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Tags: Human

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

1218837

WEST Search History

DATE: Monday, November 03, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=AND		
L1	sgf-1 or sgf1 or sgfl or sgf-l or sgfi or sgf-i	72	L1
L2	L1 and neisser$	7	L2
L3	L2 and region	7	L3
L4	L3	7	L4
L5	meningi$ and (sero$ or sera$ or $type) and l1 not l2	2	L5
L6	c751 or c-751 or z2491 or z-2491	33	L6
L7	L6 and neiss$	15	L7
L8	L7 not l2	14	L8

END OF SEARCH HISTORY

WEST Search History

DATE: Monday, November 03, 2003

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=AND		
L1	sgf-1 or sgf1 or sgfl or sgf-l or sgfi or sgf-i	72	L1
L2	L1 and neisser$	7	L2
L3	L2 and region	7	L3
L4	L3	7	L4
L5	meningi$ and (sero$ or sera$ or $type) and l1 not l2	2	L5

END OF SEARCH HISTORY

To obtain the subtractive banks, strain Z2491 of Nm (Achtman et al., 1991, J. Infect. Dis. 164, 375-382), the strains MS11 (Swanson et al., 1974, Infect. Immun. 10, 633-644) and the strains 8064 and 9764 of Nl were used, it being understood that any other strain of the species in question could be used.

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Search Results - Record(s) 1 through 14 of 14 returned.

☐ 1. 20030194116 . 10 Apr 02. 16 Oct 03. Visualization of information with an established order. Wong, Pak Chung, et al. 382/128; 382/167 382/168 G06K009/00.

☐ 2. 20030148268 . 05 Dec 02. 07 Aug 03. Novel method to identify targets for antibiotic development. Fischetti, Vincent A., et al. 435/5; 435/34 C12Q001/70 C12Q001/04.

☐ 3. 20030134904 . 23 Sep 02. 17 Jul 03. Inhibitors of RNase P proteins as antibacterial compounds. Giordano, Tony, et al. 514/614; 514/357 564/147 A61K031/165 C07C279/20.

☐ 4. 20030119061 . 28 Jun 02. 26 Jun 03. Structure-based drug design methods for identifying D-Ala-D-Ala ligase inhibitors as antibacterial drugs. Ala, Paul J., et al. 435/7.1; 702/19 G01N033/53 G06F019/00 G01N033/48 G01N033/50.

☐ 5. 20030101005 . 12 Jul 02. 29 May 03. Crystals and structures of perosamine synthase homologs. Muller-Dieckmann, Hans-Joachim, et al. 702/27; 703/11 G06F019/00 G06G007/48.

☐ 6. 20030087257 . 10 Apr 02. 08 May 03. Method for assembling of fragments in DNA sequencing. Pevzner, Pavel A., et al. 435/6; 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50.

☐ 7. 20030082591 . 24 Jul 02. 01 May 03. Methods for gene disruption and uses thereof. Awrey, Donald, et al. 435/6; 435/252.3 435/325 435/455 435/471 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50 C12N015/87 C12N015/74 C12N001/21 C12N005/06.

☐ 8. 20030073134 . 17 Jun 02. 17 Apr 03. Crystals and structures of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase MECPS. Louie, Gordon V., et al. 435/7.1; 702/19 G01N033/53 G06F019/00 G01N033/48 G01N033/50.

☐ 9. 20030054370 . 27 Feb 02. 20 Mar 03. Systematic discovery of new genes and genes discovered thereby. Zeng, Qiandong, et al. 435/6; 435/5 702/20 C12Q001/68 C12Q001/70 G06F019/00.

☐ 10. 20030022292 . 07 Jun 02. 30 Jan 03. Ligation of CEACAM1. Gray-Owen, Scott D., et al. 435/69.1; 424/184.1 C12P021/06 A61K039/00 A61K039/38.

☐ 11. 20020182630 . 07 May 02. 05 Dec 02. Comparative mapping and assembly of nucleic acid sequences. Milosavljevic, Aleksandar. 435/6; 702/20 C12Q001/68 G06F019/00 G01N033/48 G01N033/50.

☐ 12. 20020168681 . 20 Mar 01. 14 Nov 02. Microorganisms and assays for the identification of antibiotics. Yocum, R. Rogers, et al. 435/7.1; G01N033/53.

☐ 13. 20020160016 . 25 Jan 01. 31 Oct 02. Modified surface antigen. Peak, Ian Richard Anselm, et al. 424/190.1; 435/183 A61K039/095 C12N009/00.

☐ 14. 20020144309 . 08 Feb 02. 03 Oct 02. Transgenic plants expressing MinD or MinE and an efficient method for plant chloroplast transformation and gene expression. Dinkins, Randy, et al. 800/282; 435/189 435/320.1 435/419 435/69.1 A01H001/00 C12N009/02 C12P021/02 C12N005/04.

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Terms	Documents
L7 not l2	14

NCBI PubMed National Library of Medicine NLM

Entrez PubMed Nucleotide Protein Genome Structure PMC Journ

Search PubMed for z2491 1996 Preview

Limits Preview/Index History Clipboard Details

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.

Entrez PubMed

PubMed Services

Search	Most Recent Queries	Time	Result
#2	Search **z2491 1991**	09:28:42	0
#10	Search **z2491 1992**	09:28:36	0
#9	Search **z2491 1993**	09:28:27	0
#8	Search **z2491 1994**	09:28:21	0
#7	Search **z2491 1995**	09:27:51	2
#4	Search **z2491 1996**	09:25:13	2
#3	Search **z2491 achtman**	09:24:09	1
#1	Search **z2491**	09:23:38	15

Clear History

Related Resources

Search in Swiss-Prot and TrEMBL for: hsp60 neisseria

Swiss-Prot Release 42.1 of 24-Oct-2003
TrEMBL Release 25.1 of 24-Oct-2003

- Number of sequences found in Swiss-Prot$_{(2)}$ and TrEMBL$_{(0)}$: **2**
- For more directed searches, you can use the Sequence Retrieval System SRS.

Search in Swiss-Prot: There are matches to 2 out of 136356 entries

CH60_NEIMA (**P57006**)
60 kDa chaperonin (Protein Cpn60) (groEL protein) (63 kDa stress protein) (GSP63) (HSP60). {GENE: GROL OR GROEL OR MOPA OR HSP63 OR NMA0473} - Neisseria meningitidis (serogroup A)

CH60_NEIMB (**P42385**)
60 kDa chaperonin (Protein Cpn60) (groEL protein) (63 kDa stress protein) (GSP63) (HSP60). {GENE: GROL OR GROEL OR MOPA OR HSP63 OR NMB1972} - Neisseria meningitidis (serogroup B)

Search in TrEMBL: There are matches to 0 out of 1016356 entries

New Search

in Swiss-Prot/TrEMBL by AC, ID, description, gene name, organism
Please do NOT use any boolean operators (and, or, etc.)

NiceProt View of Swiss-Prot: P05838

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**SSPA_ECOLI**
Primary accession number	**P05838**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 09, November 1988
Sequence was last modified in	Release 31, February 1995
Annotations were last modified in	Release 42, October 2003

Name and origin of the protein

Protein name	**Stringent starvation protein A**
Synonyms	None
Gene name	**SSPA** or **SSP** or **POG** or **B3229** or **C3982** or **Z4587** or **ECS4102** or **SF3269** or **S3484**
From	Escherichia coli [TaxID: 562] Escherichia coli O6 [TaxID: 217992] Escherichia coli O157:H7 [TaxID: 83334] Shigella flexneri [TaxID: 623]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

[1] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
MEDLINE=87146422; PubMed=3029697; [NCBI, ExPASy, EBI, Israel, Japan]
Serizawa H., Fukuda R.;
"Structure of the gene for the stringent starvation protein of Escherichia coli.";
Nucleic Acids Res. 15:1153-1163(1987).

[2]
SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503; [NCBI, ExPASy, EBI, Israel, Japan]
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).

[3] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157; [NCBI, ExPASy, EBI, Israel, Japan]
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

[4] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551; [NCBI, ExPASy, EBI, Israel, Japan]
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).

[5] SEQUENCE FROM NUCLEIC ACID.
SPECIES=E.coli;
STRAIN=O157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796; [NCBI, ExPASy, EBI, Israel, Japan]
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).

[6] SEQUENCE OF 1-12.
SPECIES=E.coli;
STRAIN=K12 / EMG2;
MEDLINE=97443975; PubMed=9298646; [NCBI, ExPASy, EBI, Israel, Japan]
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).

[7] SEQUENCE FROM NUCLEIC ACID.
SPECIES=S.flexneri;
STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590; [NCBI, ExPASy, EBI, Israel, Japan]
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding

K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).

[8] SEQUENCE FROM NUCLEIC ACID.
SPECIES=S.flexneri;
STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152; [NCBI, ExPASy, EBI, Israel, Japan]
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).

[9] CHARACTERIZATION.
SPECIES=E.coli;
MEDLINE=94293773; PubMed=8022275; [NCBI, ExPASy, EBI, Israel, Japan]
Williams M.D., Ouyang T.X., Flickinger M.C.;
"Starvation-induced expression of SspA and SspB: the effects of a null mutation in sspA on Escherichia coli protein synthesis and survival during growth and prolonged starvation.";
Mol. Microbiol. 11:1029-1043(1994).

Comments

- ***FUNCTION***: FORMS AN EQUIMOLAR COMPLEX WITH THE RNA POLYMERASE HOLOENZYME (RNAP) BUT NOT WITH THE CORE ENZYME, IT IS SYNTHESIZED PREDOMINANTLY WHEN CELLS ARE EXPOSED TO AMINO ACID STARVATION, AT WHICH TIME IT ACCOUNTS FOR OVER 50% OF THE TOTAL PROTEIN SYNTHESIZED. IT IS INVOLVED IN THE TRANSITION FROM P1 EARLY TO P1 LATE GENE EXPRESSION. RNK AND SSPA CAN FUNCTIONALLY REPLACE P.AERUGINOSA ALGINATE REGULATORY GENE ALGR2.
- ***INDUCTION***: By amino acid starvation.
- ***SIMILARITY***: Belongs to the GST superfamily. HSP26 family.

Copyright

Cross-references

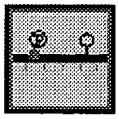
EMBL	X05088; CAA28740.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	U18997; AAA58031.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE000402; AAC76261.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE016767; AAN82422.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE005550; AAG58357.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AP002564; BAB37525.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE015337; AAN44733.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
	AE016989; AAP18544.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A26422; RGECSS.
	A85987; A85987.
	F91141; F91141.
SWISS-2DPAGE	P05838; COLI.
ECO2DBASE	D027.1; 6TH EDITION.

EcoGene	EG10977; sspA.
EcoCyc	EG10977; sspA.
CMR	P05838; B3229.
InterPro	IPR004046; GST_Cterm. IPR004045; GST_Nterm. Graphical view of domain structure.
Pfam	PF00043; GST_C; 1. PF02798; GST_N; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P05838.
ProtoNet	P05838.
ProtoMap	P05838.
PRESAGE	P05838.
DIP	P05838.
ModBase	P05838.

Keywords

Complete proteome.

Features

 Feature table viewer

Key	From	To	Length	Description
INIT_MET	0	0		

Sequence information

Length: **211** **AA** Molecular weight: **24173** **Da** CRC64: **7D4F8D6CF71AAF01** [This is a checksum on the sequence]

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        10         20         30         40         50         60
         |          |          |          |          |          |
AVAANKRSVM TLFSGPTDIY SHQVRIVLAE KGVSFEIEHV EKDNPPQDLI DLNPNQSVPT

        70         80         90        100        110        120
         |          |          |          |          |          |
LVDRELTLWE SRIIMEYLDE RFPHPPLMPV YPVARGESRL YMHRIEKDWY TLMNTIINGS

       130        140        150        160        170        180
         |          |          |          |          |          |
ASEADAARKQ LREELLAIAP VFGQKPYFLS DEFSLVDCYL APLLWRLPQL GIEFSGPGAK

       190        200        210
         |          |          |
ELKGYMTRVF ERDSFLASLT EAEREMRLGR S
```

P05838 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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sp P05838 SSPA_ECOLI **Stringent starvation protein A [SSPA] [Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri]** 211 AA align

Score = 174 bits (440), Expect = 9e-43
Identities = 92/201 (45%), Positives = 130/201 (64%), Gaps = 3/201 (1%)

```
Query: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60
           +MTL+SG T  +SH+ R VL EKG+ FEI+ V+  N P+DL  +NP   VP LV+R+L L
Sbjct: 9   VMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTL 68

Query: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120
            ES II EY+DERFPHP LMP  PV RG  RL ++R+EK+ +  +  + N +A+  E
Sbjct: 69  WESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMNTIINGSAS--EADA 126

Query: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKL-GKSAAPLLKYA 179
           AR+ +   L  +AP F +  Y L ++FS++D  LAPLLWRL    ++  G  A  L  Y
Sbjct: 127 ARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGIEFSGPGAKELKGYM 186

Query: 180 ERIFQREAFIEALTPAEKAMR 200
            R+F+R++F+ +LT AE+ MR
Sbjct: 187 TRVFERDSFLASLTEAEREMR 207
```

tr O33374 **RegF protein [REGF] [Neisseria gonorrhoeae]** 201 AA
align

Score = 401 bits (1030), Expect = e-111
Identities = 197/201 (98%), Positives = 199/201 (99%)

```
Query: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60
           MMTLYSGITCPFSHRCRFVLYEKGMDFEIKD+DIYNKPEDLAVMNPYNQVPVLVERDLVL
Sbjct: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDIDIYNKPEDLAVMNPYNQVPVLVERDLVL 60

Query: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120
           HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAA NKEQAK
Sbjct: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAAANKEQAK 120

Query: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKLGKSAAPLLKYAE 180
           AREAIGNGLTML+PSFSKSKYILGEDFSMIDVALAPLLWRL HYDVKLGKSAAPLLKYAE
Sbjct: 121 AREAIGNGLTMLSPSFSKSKYILGEDFSMIDVALAPLLWRLDHYDVKLGKSAAPLLKYAE 180

Query: 181 RIFQREAFIEALTPAEKAMRK 201
           RIFQREAFIEALTPAEKAMRK
Sbjct: 181 RIFQREAFIEALTPAEKAMRK 201
```

trnew AAQ61667 **Stringent starvation protein A [sspA] [Chromobacterium violaceum ATCC 12472]** 200 AA
align

Score = 325 bits (833), Expect = 2e-88
Identities = 158/201 (78%), Positives = 178/201 (88%), Gaps = 1/201 (0%)

```
Query: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60
           MMTLYSGITCPFS RCR VL+EKGMDFEI DVDI+NKPEDLAVMNPYN+VPVLVERDL+L
Sbjct: 1   MMTLYSGITCPFSQRCRIVLFEKGMDFEIIDVDIHNKPEDLAVMNPYNEVPVLVERDLIL 60

Query: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120
           HESNIINEYIDERFPHPQLMP DPVMR R RL LYR E ELF HV+ LE   AT KE  K
Sbjct: 61  HESNIINEYIDERFPHPQLMPADPVMRARARLFLYRFENELFIHVKTLE-AGATGKEATK 119

Query: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKLGKSAAPLLKYAE 180
           AREAI +GLT +AP FSK K++LG+DFSMIDVA+APL+WRL HY++ LGKSAAP+LKYAE
Sbjct: 120 AREAIRDGLTTIAPIFSKQKFMLGDDFSMIDVAIAPLMWRLEHYNIDLGKSAAPILKYAE 179

Query: 181 RIFQREAFIEALTPAEKAMRK 201
           RIFQR++FI++LTP+EKAMRK
Sbjct: 180 RIFQRQSFIDSLTPSEKAMRK 200
```

trnew CAE16385 **Stringent starvation protein A [sspA] [Photorhabdus luminescens subsp. laumondii TTO1]** 213 AA
align

Score = 174 bits (442), Expect = 5e-43
Identities = 89/201 (44%), Positives = 133/201 (66%), Gaps = 3/201 (1%)

```
Query: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60
```

```
           +MTL+SG    FSH+ R VL EKG+  E++ V+  N P+DL  +NPY  VP LV+R+L L
Sbjct: 10  VMTLFSGPADIFSHQVRIVLAEKGVSVEVEQVEAGNLPQDLIDLNPYQTVPTLVDRELTL 69

Query: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120
           ++S II EY+DERFPHP LMP  PV RG  RL+++R+EK+ ++ +  +E     ++E
Sbjct: 70  YDSRIIMEYLDERFPHPPLMPVYPVARGSSRLMMHRIEKDWYSLMHTIEK--GNSQEANT 127

Query: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKLGKSAAPLLK-YA 179
           AR+ +   L  +AP F +  + + E+FS++D  LAPLLWRL    ++L  S    L+ Y
Sbjct: 128 ARKRLAEELLAVAPIFKEMPFFMSEEFSLVDCYLAPLLWRLPVLGIELPSSGTKDLQIYM 187

Query: 180 ERIFQREAFIEALTPAEKAMR 200
           +R+F+R+AF+ +LT AE+ MR
Sbjct: 188 QRVFERDAFLASLTEAEREMR 208
```

sp P05838 SSPA_ECOLI **Stringent starvation protein A [SSPA] [Escherichia coli, Escherichia coli O6, Escherichia coli O157:H7, Shigella flexneri]** 211 AA align

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 Score =  174 bits (440), Expect = 9e-43
 Identities = 92/201 (45%), Positives = 130/201 (64%), Gaps = 3/201 (1%)

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Query: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120
            ES II EY+DERFPHP LMP  PV RG  RL ++R+EK+ +  +  + N +A+  E
Sbjct: 69  WESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMNTIINGSAS--EADA 126

Query: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKL-GKSAAPLLKYA 179
           AR+ +   L  +AP F +  Y L ++FS++D  LAPLLWRL    ++  G  A  L  Y
Sbjct: 127 ARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGIEFSGPGAKELKGYM 186

Query: 180 ERIFQREAFIEALTPAEKAMR 200
            R+F+R++F+ +LT AE+ MR
Sbjct: 187 TRVFERDSFLASLTEAEREMR 207
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CLUSTAL FORMAT for T-COFFEE Version_1.37, CPU=0.10 sec, SCORE=4210, Nseq=2, Len=213

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sp|P05838|SSPA_ECOLI           AVAANKRSVMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNP
                                       :***:** *  :**: *:** ***:.***:.*:  * *:**  :**

unk|VIRT5619|Blast_submission  LVERDLVLHESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQ
sp|P05838|SSPA_ECOLI           LVDRELTLWESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMN
                               **:*:*.* **.** **:******* ***  ** **..** ::*:**: :. ::

unk|VIRT5619|Blast_submission  ATNKEQAKAREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDV
sp|P05838|SSPA_ECOLI           AS--EADAARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGI
                               *:  *   **: : : *  :** *.:. *:*.::**::*  ******** : .:

unk|VIRT5619|Blast_submission  AAPLLKYAERIFQREAFIEALTPAEKAMRK---
sp|P05838|SSPA_ECOLI           AKELKGYMTRVFERDSFLASLTEAEREMRLGRS
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Cold

ArgJ

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SV   M65216.1
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DT   04-MAR-2000 (Rel. 63, Last updated, Version 3)
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DE   Neisseria gonorrhoeae ornithine acetyltransferase (argJ) gene, complete
DE   cds.
XX
KW   ornithine acetyltransferase.
XX
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OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
OC   Neisseria.
XX
RN   [1]
RP   1-1500
RX   MEDLINE; 92210515.
RX   PUBMED; 1339419.
RA   Martin P.R., Mulks M.H.;
RT   "Sequence analysis and complementation studies of the argJ gene encoding
RT   ornithine acetyltransferase from Neisseria gonorrhoeae";
RL   J. Bacteriol. 174(8):2694-2701(1992).
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DR   SWISS-PROT; P38434; ARGJ_NEIGO.
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DT   17-MAR-2000 (Rel. 63, Last updated, Version 2)
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XX
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OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae;
OC   Neisseria.
XX
RN   [1]
RC   GenBank staff at the National Library of Medicine created this entry [NCBI
RC   gibbsq 85363] from the original journal article. This sequence comes from
RC   Figure 3.
RP   1-1221
RX   MEDLINE; 92176016.
RX   PUBMED; 1339413.
RA   Martin P.R., Mulks M.H.;
RT   "Molecular characterization of the argJ mutation in Neisseria gonorrhoeae
RT   strains with requirements for arginine, hypoxanthine, and uracil";
RL   Infect. Immun. 60(3):970-975(1992).
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DR   GOA; P38434.
DR   SWISS-PROT; P38434; ARGJ_NEIGO.
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NiceProt View of Swiss-Prot: Q9JRJ2

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[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**ARGJ_NEIMA**
Primary accession number	**Q9JRJ2**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 42, October 2003
Sequence was last modified in	Release 42, October 2003
Annotations were last modified in	Release 42, October 2003

Name and origin of the protein

Protein name	**Arginine biosynthesis bifunctional protein argJ**
Synonyms	None
Includes	**Glutamate N-acetyltransferase** (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase) **Amino-acid acetyltransferase** (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)
Contains	**Arginine biosynthesis bifunctional protein argJ alpha chain** **Arginine biosynthesis bifunctional protein argJ beta chain**
Gene name	**ARGJ** or **NMA0435** or **NMB2005**
From	Neisseria meningitidis (serogroup A) [TaxID: 65699] Neisseria meningitidis (serogroup B) [TaxID: 491]
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

References

[1] SEQUENCE FROM NUCLEIC ACID.

STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919; [NCBI, ExPASy, EBI, Israel, Japan]
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
Nature 404:502-506(2000).

[2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307; [NCBI, ExPASy, EBI, Israel, Japan]
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
Science 287:1809-1815(2000).

Comments

- ***FUNCTION***: Catalyzes two activities which are involved in the cyclic version of arginine biosynthesis: the synthesis of acetylglutamate from glutamate and acetyl-CoA, and of ornithine by transacetylation between acetylornithine and glutamate *(By similarity)*.
- ***CATALYTIC ACTIVITY***: N^2-acetyl-L-ornithine + L-glutamate = L-ornithine + N-acetyl-L-glutamate.
- ***CATALYTIC ACTIVITY***: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-glutamate.
- ***PATHWAY***: Arginine biosynthesis; first step.
- ***PATHWAY***: Arginine biosynthesis; fifth step.
- ***SUBUNIT***: Heterotetramer of two alpha and two beta chains *(By similarity)*.
- ***SUBCELLULAR LOCATION***: Cytoplasmic *(Probable)*.
- ***MISCELLANEOUS***: Some bacteria possess a monofunctional argJ, i.e., capable of catalyzing only the fifth step of the arginine biosynthetic pathway.
- ***SIMILARITY***: Belongs to the argJ family.

Copyright

Cross-references

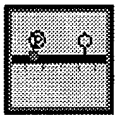
EMBL	AL162753; CAB83734.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] AE002550; AAF42332.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	C81017; C81017.
TIGR	NMB2005; -.
HAMAP	MF_01106; -; 1. PBIL [Family / Alignment / Tree]
InterPro	IPR002813; ArgJ. Graphical view of domain structure.
Pfam	PF01960; ArgJ; 1.
ProDom	PD004193; ArgJ; 1.

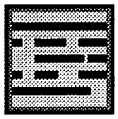
	[Domain structure / List of seq. sharing at least 1 domain]
TIGRFAMs	TIGR00120; ArgJ; 1.
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	Q9JRJ2.
ProtoNet	Q9JRJ2.
ProtoMap	Q9JRJ2.
PRESAGE	Q9JRJ2.
DIP	Q9JRJ2.
ModBase	Q9JRJ2.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Arginine biosynthesis; **Multifunctional enzyme**; **Transferase**; **Acyltransferase**; **Complete proteome**.

Features

 Feature table viewer

 Feature aligner

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CHAIN	190	406	217	ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ BETA CHAIN (*BY SIMILARITY*).
SITE	189	190	2	CLEAVAGE (NONHYDROLYTIC) (*BY SIMILARITY*).

Sequence information

Length: **406 AA** [This is the length of the unprocessed precursor]

Molecular weight: **42811 Da** [This is the MW of the unprocessed precursor]

CRC64: **0915D50CE69CA656** [This is a checksum on the sequence]

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Q9JRJ2 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot

Hosted by NCSC US | Mirror sites: Bolivia | Canada | China | Korea | Switzerland | Taiwan

NiceProt View of Swiss-Prot: P38434

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**ARGJ_NEIGO**
Primary accession number	**P38434**
Secondary accession number	Q53567
Entered in Swiss-Prot in	Release 30, October 1994
Sequence was last modified in	Release 30, October 1994
Annotations were last modified in	Release 42, October 2003

Name and origin of the protein

Protein name	**Arginine biosynthesis bifunctional protein argJ**
Synonyms	None
Includes	**Glutamate N-acetyltransferase** (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase) **Amino-acid acetyltransferase** (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)
Contains	**Arginine biosynthesis bifunctional protein argJ alpha chain** **Arginine biosynthesis bifunctional protein argJ beta chain**
Gene name	**ARGJ**
From	Neisseria gonorrhoeae [TaxID: 485]
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=CDC 50;

MEDLINE=92210515; PubMed=1339419; [NCBI, ExPASy, EBI, Israel, Japan]
Martin P.R., Mulks M.H.;
"Sequence analysis and complementation studies of the argJ gene encoding ornithine acetyltransferase from Neisseria gonorrhoeae.";
J. Bacteriol. 174:2694-2701(1992).

[2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=NRL 30465;
MEDLINE=92176016; PubMed=1339413; [NCBI, ExPASy, EBI, Israel, Japan]
Martin P.R., Mulks M.H.;
"Molecular characterization of the argJ mutation in Neisseria gonorrhoeae strains with requirements for arginine, hypoxanthine, and uracil.";
Infect. Immun. 60:970-975(1992).

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- ***CATALYTIC ACTIVITY***: Acetyl-CoA + L-glutamate = CoA + N-acetyl-L-glutamate.
- ***PATHWAY***: Arginine biosynthesis; first step.
- ***PATHWAY***: Arginine biosynthesis; fifth step.
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- ***SUBCELLULAR LOCATION***: Cytoplasmic.
- ***MISCELLANEOUS***: Some bacteria possess a monofunctional argJ, i.e., capable of catalyzing only the fifth step of the arginine biosynthetic pathway.
- ***SIMILARITY***: Belongs to the argJ family.

Copyright

Cross-references

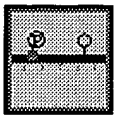
EMBL	M65216; AAA25447.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] S85363; AAB21605.2; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A43850; A43850.
HAMAP	MF_01106; -; 1. PBIL [Family / Alignment / Tree]
InterPro	IPR002813; ArgJ. Graphical view of domain structure.
Pfam	PF01960; ArgJ; 1.
ProDom	PD004193; ArgJ; 1. [Domain structure / List of seq. sharing at least 1 domain]
TIGRFAMs	TIGR00120; ArgJ; 1.
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P38434.
ProtoNet	P38434.
ProtoMap	P38434.
PRESAGE	P38434.

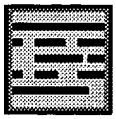
DIP P38434.
ModBase P38434.
SWISS-2DPAGE Get region on 2D PAGE.

Keywords

Arginine biosynthesis; **Multifunctional enzyme**; **Transferase**; **Acyltransferase**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description
CHAIN	1	189	189	ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ ALPHA CHAIN (*BY SIMILARITY*).
CHAIN	190	406	217	ARGININE BIOSYNTHESIS BIFUNCTIONAL PROTEIN ARGJ BETA CHAIN (*BY SIMILARITY*).
SITE	189	190	2	CLEAVAGE (NONHYDROLYTIC) (*BY SIMILARITY*).
CONFLICT	120	120		G -> A (IN REF. 2).

Sequence information

Length: **406 AA** [This is the length of the unprocessed precursor]

Molecular weight: **42865 Da** [This is the MW of the unprocessed precursor]

CRC64: **5515EA4EB7503814** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
         |          |          |          |          |          |
MAVNLTEKTA EQLPDIDGIA LYTAQAGVKK PGHTDLTLIA VAAGSTVGAV FTTNRFCAAP

        70         80         90        100        110        120
         |          |          |          |          |          |
VHIAKSHLFD EDGVRALVIN TGNANAGTGA QGRIDALAVC AAAARQIGCK PNQVMPFSTG

       130        140        150        160        170        180
         |          |          |          |          |          |
VILEPLPADK IIAALPKMQP AFWNEAARAI MTTDTVPKAA SREGKVGDQH TVRATGIAKG

       190        200        210        220        230        240
         |          |          |          |          |          |
SGMIHPNMAT MLGFIATDAK VSQPVLQLMT QEIADETFNT ITVDGDTSTN DSFVIIATGK

       250        260        270        280        290        300
         |          |          |          |          |          |
NSQSEIDNIA DPRYAQLKEL LCSLALELAQ AIVRDGEGAT KFITVRVENA KTCDEARQAA

       310        320        330        340        350        360
         |          |          |          |          |          |
YAAARSPLVK TAFFASDPNL GKRLAAIGYA DVADLDTDLV EMYLDDILVA EHGGRAASYT

       370        380        390        400
         |          |          |          |
EAQGQAVMSK DEITVRIKLH RGQAAATVYT CDLSHGYVSI NADYRS
```

P38434 in FASTA format

View entry in original Swiss-Prot format
View entry in raw text format (no links)
Report form for errors/updates in this Swiss-Prot entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot

Hosted by NCSC US | Mirror sites: Bolivia | Canada | China | Korea | Switzerland | Taiwan

sp P38434 ARGJ_NEIGO **Arginine biosynthesis bifunctional protein argJ [Includes: Glutamate N-acetyltransferase (EC 2.3.1.35) (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase); Amino-acid acetyltransferase (EC 2.3.1.1) (N-acetylglutamate synthase) (AGS)] [Contains: Arginine biosynthesis bifunctional protein argJ alpha chain; Arginine biosynthesis bifunctional protein argJ beta chain] [ARGJ] [Neisseria gonorrhoeae]** 406 AA align

Score = 714 bits (1843), Expect = 0.0
Identities = 370/406 (91%), Positives = 373/406 (91%)

```
Query: 1   MAVNLTEKTAEQLPDIDGIALYTAQAGVKKPGHTDLTLIAVAAGSTVGAVFTTNRFCAAP 60
           MAVNLTEKTAEQLPDIDGIALYTAQAGVKKPGHTDLTLIAVAAGSTVGAVFTTNRFCAAP
Sbjct: 1   MAVNLTEKTAEQLPDIDGIALYTAQAGVKKPGHTDLTLIAVAAGSTVGAVFTTNRFCAAP 60

Query: 61  VHIAKSHLFDEDGVRALVIXXXXXXXXXXQGRIDALAVCAAAARQIGCKPNQVLPFSTG 120
           VHIAKSHLFDEDGVRALVI           QGRIDALAVCAAAARQIGCKPNQV+PFSTG
Sbjct: 61  VHIAKSHLFDEDGVRALVINTGNANAGTGAQGRIDALAVCAAAARQIGCKPNQVMPFSTG 120

Query: 121 VILEPLPADKIIAALPKMQPAFWNEAARAIMTTDTVPKAASREGKVGDKHTVRATGIAKG 180
           VILEPLPADKIIAALPKMQPAFWNEAARAIMTTDTVPKAASREGKVGD+HTVRATGIAKG
Sbjct: 121 VILEPLPADKIIAALPKMQPAFWNEAARAIMTTDTVPKAASREGKVGDQHTVRATGIAKG 180

Query: 181 SGMIHPNMATMLGFIATDAKVSQPVLQLMTQEIADETFNTITVDGDTSTNDSFVIIATGK 240
           SGMIHPNMATMLGFIATDAKVSQPVLQLMTQEIADETFNTITVDGDTSTNDSFVIIATGK
Sbjct: 181 SGMIHPNMATMLGFIATDAKVSQPVLQLMTQEIADETFNTITVDGDTSTNDSFVIIATGK 240

Query: 241 NSQSEIDNIADPRYXXXXXXXXXXXXXXXXXIVRDGEGATKFITVRVENAKTRDEARQAA 300
           NSQSEIDNIADPRY                 IVRDGEGATKFITVRVENAKT DEARQAA
Sbjct: 241 NSQSEIDNIADPRYAQLKELLCSLALELAQAIVRDGEGATKFITVRVENAKTCDEARQAA 300

Query: 301 YAVARSPLVKTAFFASDPNLGRLLAAIGYAGVADLDTDLVEMYLDDILVAEHGGRAASYT 360
           YA ARSPLVKTAFFASDPNLG+ LAAIGYA VADLDTDLVEMYLDDILVAEHGGRAASYT
Sbjct: 301 YAAARSPLVKTAFFASDPNLGKRLAAIGYADVADLDTDLVEMYLDDILVAEHGGRAASYT 360

Query: 361 EAQGQAVMSKAEITVRIKLHRGQAAATVYTCDLSHGYVSINADYRS 406
           EAQGQAVMSK EITVRIKLHRGQAAATVYTCDLSHGYVSINADYRS
Sbjct: 361 EAQGQAVMSKDEITVRIKLHRGQAAATVYTCDLSHGYVSINADYRS 406
```

NiceProt View of Swiss-Prot: P38367

Entry information

Entry name	**OMP4_NEIMA**
Primary accession number	**P38367**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 30, October 1994
Sequence was last modified in	Release 40, October 2001
Annotations were last modified in	Release 40, October 2001

Name and origin of the protein

Protein name	**Outer membrane protein class 4 [Precursor]**
Synonyms	None
Gene name	**RMPM** or **NMA2105** or **NMB0382**
From	Neisseria meningitidis (serogroup A) [TaxID: 65699] Neisseria meningitidis (serogroup B) [TaxID: 491]
Taxonomy	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

References

[1] SEQUENCE FROM NUCLEIC ACID.
STRAIN=CCUG 18241 / M986 / Serogroup B / Serotype 2;
MEDLINE=89277523; PubMed=2499543; [NCBI, ExPASy, EBI, Israel, Japan]
Klugman K.P., Gotschlich E.C., Blake M.S.;
"Sequence of the structural gene (rmpM) for the class 4 outer membrane protein of Neisseria meningitidis, homology of the protein to gonococcal protein III and Escherichia coli OmpA, and construction of meningococcal strains that lack class 4 protein.";
Infect. Immun. 57:2066-2071(1989).

[2] SEQUENCE FROM NUCLEIC ACID.
STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919; [NCBI, ExPASy, EBI, Israel, Japan]
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D.,

Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
Nature 404:502-506(2000).

[3] SEQUENCE FROM NUCLEIC ACID.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307; [NCBI, ExPASy, EBI, Israel, Japan]
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
Science 287:1809-1815(2000).

Comments

- ***SUBCELLULAR LOCATION***: Integral membrane protein. Outer membrane.
- ***SIMILARITY***: BELONGS TO THE OMPA FAMILY. STRONG, TO N.GONORRHOEAE P.III.

Copyright

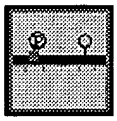
Cross-references

EMBL	AL162758; CAB85320.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence] AE002394; AAF40822.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A37004; A37004. A81782; A81782. C81205; C81205.
TIGR	NMB0382; -.
InterPro	IPR006664; Bac_OmpA. IPR006665; OmpA/MotB. IPR006690; OMPA_LIKE. Graphical view of domain structure.
Pfam	PF00691; OmpA; 1.
PRINTS	PR01021; OMPADOMAIN.
ProDom	PD000930; OmpA/MotB; 1. [Domain structure / List of seq. sharing at least 1 domain]
PROSITE	PS01068; OMPA; 1.
HOBACGEN	[Family / Alignment / Tree]
BLOCKS	P38367.
ProtoNet	P38367.
ProtoMap	P38367.
PRESAGE	P38367.
DIP	P38367.
ModBase	P38367.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Outer membrane; Porin; Transmembrane; Signal; Repeat; Complete proteome.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description
SIGNAL	1	22	22	*POTENTIAL.*
CHAIN	23	242	220	OUTER MEMBRANE PROTEIN CLASS 4.
DOMAIN	69	82	14	7 X 2 AA TANDEM REPEATS OF X-P.
REPEAT	69	70	2	1.
REPEAT	71	72	2	2.
REPEAT	73	74	2	3.
REPEAT	75	76	2	4.
REPEAT	77	78	2	5.
REPEAT	79	80	2	6.
REPEAT	81	82	2	7.
DOMAIN	137	181	45	OMPA-LIKE.
DISULFID	191	214		*BY SIMILARITY.*
VARIANT	78	79	2	MISSING (IN STRAIN CCUG 18241).
VARIANT	128	129	2	GQ -> SR (IN STRAIN MC58).
VARIANT	132	132	1	I -> V (IN STRAIN MC58).

Sequence information

Length: **242 AA** [This is the length of the unprocessed precursor]

Molecular weight: **26140 Da** [This is the MW of the unprocessed precursor]

CRC64: **5CCAA490236B1D62** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
         |          |          |          |          |          |
MTKQLKLSAL FVALLASGTA VAGEASVQGY TVSGQSNEIV RNNYGECWKN AYFDKASQGR

        70         80         90        100        110        120
         |          |          |          |          |          |
VECGDAVAAP EPEPEPEPAP APVVVVEQAP QYVDETISLS AKTLFGFDKD SLRAEAQDNL

       130        140        150        160        170        180
         |          |          |          |          |          |
KVLAQRLGQT NIQSVRVEGH TDFMGSDKYN QALSERRAYV VANNLVSNGV PVSRISAVGL

       190        200        210        220        230        240
         |          |          |          |          |          |
GESQAQMTQV CEAEVAKLGA KVSKAKKREA LIACIEPDRR VDVKIRSIVT RQVVPAHNHH
```

QH

P38367 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Search the SWISS-MODEL Repository

ExPASy Home page	Site Map	Search ExPASy	Contact us	Swiss-Prot

Hosted by NCSC US | Mirror sites: Bolivia | Canada | China | Korea | Switzerland | Taiwan

tr Q9JXN8 **Stringent starvation protein A [NMB1953] [Neisseria meningitidis (serogroup B)]** 201 AA align

Score = 174 bits (441), Expect = 7e-43
Identities = 92/201 (45%), Positives = 130/201 (64%), Gaps = 3/201 (1%)

```
Query: 9   VMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTL 68
           +MTL+SG T  +SH+ R VL EKG+ FEI+ V+  N P+DL  +NP   VP LV+R+L L
Sbjct: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60

Query: 69  WESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMNTIINGSAS--EADA 126
            ES II EY+DERFPHP LMP  PV RG  RL ++R+EK+ +  +  + N +A+  E
Sbjct: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120

Query: 127 ARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGIEFSGPGAKELKGYM 186
           AR+ +   L  +AP F +  Y L ++FS++D  LAPLLWRL    ++  G  A  L  Y
Sbjct: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLDHYDVKL-GKSAAPLLKYA 179

Query: 187 TRVFERDSFLASLTEAEREMR 207
            R+F+R++F+ +LT AE+ MR
Sbjct: 180 ERIFQREAFIEALTPAEKAMR 200
```

tr Q9JW85 **Putative regulator of pilE expression [REGF] [Neisseria meningitidis (serogroup A)]** 201 AA align

Score = 174 bits (440), Expect = 1e-42
Identities = 92/201 (45%), Positives = 130/201 (64%), Gaps = 3/201 (1%)

```
Query: 9   VMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTL 68
           +MTL+SG T  +SH+ R VL EKG+ FEI+ V+  N P+DL  +NP   VP LV+R+L L
Sbjct: 1   MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDVDIYNKPEDLAVMNPYNQVPVLVERDLVL 60

Query: 69  WESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMNTIINGSAS--EADA 126
            ES II EY+DERFPHP LMP  PV RG  RL ++R+EK+ +  +  + N +A+  E
Sbjct: 61  HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAATNKEQAK 120

Query: 127 ARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGIEFSGPGAKELKGYM 186
           AR+ +   L  +AP F +  Y L ++FS++D  LAPLLWRL    ++  G  A  L  Y
Sbjct: 121 AREAIGNGLTMLAPSFSKSKYILGEDFSMIDVALAPLLWRLGHYDVKL-GKSAAPLLKYA 179

Query: 187 TRVFERDSFLASLTEAEREMR 207
            R+F+R++F+ +LT AE+ MR
Sbjct: 180 ERIFQREAFIEALTPAEKAMR 200
```

tr O33374 **RegF protein [REGF] [Neisseria gonorrhoeae]** 201 AA align

Score = 172 bits (437), Expect = 2e-42
Identities = 90/201 (44%), Positives = 130/201 (64%), Gaps = 3/201 (1%)

```
Query: 9   VMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTL 68
```

```
            +MTL+SG T  +SH+ R VL EKG+ FEI+ ++  N P+DL  +NP   VP LV+R+L L
Sbjct: 1    MMTLYSGITCPFSHRCRFVLYEKGMDFEIKDIDIYNKPEDLAVMNPYNQVPVLVERDLVL 60

Query: 69   WESRIIMEYLDERFPHPPLMPVYPVARGESRLYMHRIEKDWYTLMNTIINGSAS--EADA 126
             ES II EY+DERFPHP LMP  PV RG  RL ++R+EK+ +  +  + N +A+  E
Sbjct: 61   HESNIINEYIDERFPHPQLMPGDPVMRGRGRLVLYRMEKELFNHVQVLENPAAANKEQAK 120

Query: 127  ARKQLREELLAIAPVFGQKPYFLSDEFSLVDCYLAPLLWRLPQLGIEFSGPGAKELKGYM 186
            AR+ +   L  ++P F +  Y L ++FS++D  LAPLLWRL    ++  G  A  L  Y
Sbjct: 121  AREAIGNGLTMLSPSFSKSKYILGEDFSMIDVALAPLLWRLDHYDVKL-GKSAAPLLKYA 179

Query: 187  TRVFERDSFLASLTEAEREMR 207
             R+F+R++F+ +LT AE+ MR
Sbjct: 180  ERIFQREAFIEALTPAEKAMR 200
```

Comparative characterization of the iga gene encoding IgA1 protease in Neisseria meningitidis, Neisseria gonorrhoeae and Haemophilus influenzae.

Lomholt H; Poulsen K; Kilian M

Institute of Medical Microbiology, University of Aarhus, Denmark.

Molecular microbiology (ENGLAND) Feb 1995, 15 (3) p495-506, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Cloning and sequencing of the IgA1 protease gene (iga) from **Neisseria** meningitidis strain HF13 showed an overall structure equivalent to iga genes from **Neisseria** gonorrhoeae and Haemophilus influenzae, although no region corresponding to the gonococcal alpha-peptide was evident. An additional 18 N. meningitidis and 3 H. influenzae iga genes were amplified by the polymerase chain reaction technique and sequenced corresponding approximately to the N-terminal half of the mature enzyme. Comparative analyses of a total of 29 iga genes showed that pathogenic **Neisseria** have iga genes with a significantly lower degree of heterogeneity than H. influenzae iga genes. Recombinational events indicated by mosaic-like structures corresponding to those found among N. gonorrhoeae protease genes were detected among N. meningitidis iga genes. One region showed characteristic differences in sequence and length which correlated with each of the different cleavage specificities. Meningococci were extremely conserved in this region with no evidence of recombination between isolates of different cleavage specificities. Sequences further downstream showed no obvious relationship with enzyme cleavage type. This region consisted of conserved areas interspersed with highly variable areas. Amino acid sequence homologies in the variable regions of meningococci reflected the antigenic types defined by using polyclonal neutralizing antibodies.

Tags: Comparative Study; Support, Non-U.S. Gov't

Descriptors: Bacterial Proteins--genetics--GE; *Genes, Structural, Bacterial; *Haemophilus influenzae--genetics--GE; * **Neisseria** gonorrhoeae --genetics--GE; * **Neisseria** meningitidis--genetics--GE; * **Serine Endopeptidases --genetics** --GE; Amino Acid Sequence; Base Sequence; Cloning, Molecular; Immunoglobulin A--metabolism--ME; Molecular Sequence Data; Polymorphism (Genetics); Sequence Alignment; Sequence Homology; Species Specificity; Substrate Specificity

Molecular Sequence Databank No.: GENBANK/X82467; GENBANK/X82468; GENBANK/X82469; GENBANK/X82470; GENBANK/X82471; GENBANK/X82472; GENBANK/X82473; GENBANK/X82474; GENBANK/X82475; GENBANK/X82476; GENBANK/X82477; GENBANK/X82478; GENBANK/X82479; GENBANK/X82480; GENBANK/X82481; GENBANK/X82482; GENBANK/X82483; GENBANK/X82484; GENBANK/X82485; GENBANK/X82486; GENBANK/X82487; GENBANK/X82488

CAS Registry No.: 0 (Bacterial Proteins); 0 (Immunoglobulin A)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Gene Symbol: iga

Record Date Created: 19950719

Record Date Completed: 19950719

9/9/18

DIALOG(R)File 155:MEDLINE(R)

08590412 95278726 PMID: 7758939

C-terminal glycine-histidine tagging of the outer membrane protein Iga beta of Neisseria **gonorrhoeae.**

Strauss A; Pohlner J; Klauser T; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tubingen, Germany.

FEMS microbiology letters (NETHERLANDS) Apr 1 1995, 127 (3) p249-54, ISSN 0378-1097 Journal Code: 7705721

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed
Subfile: INDEX MEDICUS

A glycine-histidine tag (Gly3His6) was added to the C-terminus of a fusion protein consisting of the cholera toxin B-subunit (CtxB) and the IgA protease beta-domain (Iga beta). The aim was to facilitate single-step purification and to create a suitable tool for kinetic and structural studies on Iga beta-driven protein translocation across the outer membrane of Gram-negative bacteria. We demonstrate that the glycine-histidine tag does not interfere with the assembly of Iga beta in the outer membrane and that the translocator function of the modified Iga beta is maintained. The applicability of the new construct for the dissection of the Iga beta mediated translocation process and general aspects of C-terminal histidine tagging of outer membrane proteins are discussed.

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--genetics--GE; *Cholera Toxin--genetics--GE; * **Neisseria** gonorrhoeae--genetics--GE; * **Serine Endopeptidases --genetics** --GE; Amino Acid Sequence; Base Sequence; Biological Transport, Active; Cell Membrane--metabolism--ME; DNA, Bacterial --genetics--GE; Dipeptides--genetics--GE; Molecular Sequence Data; **Neisseria** gonorrhoeae--metabolism--ME; Plasmids--genetics--GE; Recombinant Fusion Proteins--genetics--GE; Sequence Tagged Sites

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (DNA, Bacterial); 0 (Dipeptides); 0 (Plasmids); 0 (Recombinant Fusion Proteins); 2489-13-6 (glycylhistidine); 9012-63-9 (Cholera Toxin)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19950629

Record Date Completed: 19950629

9/9/19

DIALOG(R)File 155:MEDLINE(R)

08561303 95249604 PMID: 7732025

Peptide mimicry of the meningococcal group C capsular polysaccharide.

Westerink M A; Giardina P C; Apicella M A; Kieber-Emmons T

Department of Medicine, Medical College of Ohio, Toledo 43699, USA.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Apr 25 1995, 92 (9) p4021-5, ISSN 0027-8424 Journal Code: 7505876

Contract/Grant No.: AI26279; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Sequence analysis of the variable regions of the heavy and light chains of the anti-idiotypic antibody 6F9, which mimics the meningococcal group C capsular polysaccharide (MCP), was performed. The immunogenic site on 6F9 responsible for inducing an anti-MCP antibody response was determined by means of sequence and computer model analysis of these data. Complementarity-determining region 3 (CDR3) was found to be unique in that the sequence tract YRY was exposed on the surface. A synthetic peptide spanning the CDR3 domain was synthesized and complexed to proteosomes (meningococcal group B outer membrane protein). Immunizations of BALB/c mice with the peptide-proteosome complex resulted in a significant anti-MCP antibody response. Immunized mice were protected against infection with a lethal dose of **Neisseria** meningitidis serogroup C.

Tags: Animal; Comparative Study; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Antibodies, Anti-Idiotypic--chemistry--CH; *Immunoglobulin Variable Region--chemistry--CH; *Immunoglobulins, Heavy-Chain--chemistry --CH; *Immunoglobulins, Light-Chain--chemistry--CH; * **Neisseria** meningitidis--immunology--IM; *Polysaccharides, Bacterial--chemistry--CH; *Polysaccharides, Bacterial--immunology--IM; *Protein Structure, Secondary ; Amino Acid Sequence; Antibodies, Anti-Idiotypic--immunology--IM; Bacterial Outer Membrane Proteins--immunology--IM; Computer Simulation; Cysteine **Endopeptidases** --immunology--IM; Immunoglobulin Variable Region

--immunology--IM; Immunoglobulins, Heavy-Chain--immunology--IM; Immunoglobulins, Light-Chain--immunology--IM; Mice; Mice, Inbred BALB C; Models, Molecular; Molecular Sequence Data; Multienzyme Complexes--immunology--IM; **Neisseria** meningitidis--classification--CL; Sequence Homology, Amino Acid
CAS Registry No.: 0 (Antibodies, Anti-Idiotypic); 0 (Bacterial Outer Membrane Proteins); 0 (Immunoglobulin Variable Region); 0 (Immunoglobulins, Heavy-Chain); 0 (Immunoglobulins, Light-Chain); 0 (Multienzyme Complexes); 0 (Polysaccharides, Bacterial)
Enzyme No.: EC 3.4.22 (Cysteine **Endopeptidases**); EC 3.4.99.46 (multicatalytic endopeptidase complex)
Record Date Created: 19950601
Record Date Completed: 19950601

9/9/20
DIALOG(R)File 155:MEDLINE(R)

08492486 95180702 PMID: 7875573
Identification and characterization of specific sequences encoding pathogenicity associated proteins in the genome of commensal Neisseria **species.**
Wolff K; Stern A
Department of Biotechnology, TB-Z, Boehringer Mannheim GmbH, Penzberg, Germany.
FEMS microbiology letters (NETHERLANDS) Jan 15 1995, 125 (2-3) p255-63, ISSN 0378-1097 Journal Code: 7705721
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The distribution of distinct sequences in pathogenic and commensal **Neisseria** species was investigated systematically by dot blot analysis. Probes representing the genes of Rmp, pilin and IgA1 protease were found to hybridize exclusively to the chromosomal DNA of the pathogenic species, **Neisseria** gonorrhoeae and/or **Neisseria** meningitidis. In contrast, specific sequences for the genes of the porin protein Por and the opacity protein (Opa) were also detected in a panel of commensal **Neisseria** species such as N. lactamica, N. subflava, N. flava, N. mucosa and N. sicca. Using opa-specific oligonucleotides as probes in chromosomal blots, the genomes of the commensal **Neisseria** species show a totally reduced repertoire of cross-hybridizing loci compared to the complex opa gene family of N. gonorrhoeae. DNA sequence analysis of one opa-related gene derived from N. flava and N. sicca, respectively, revealed a large degree of homology with previously described gonococcal and meningococcal genes, e.g., a typical repetitive sequence in the leader peptide and the distribution of the hypervariable and conserved regions. This observation, together with the finding, that the gene is constitutively transcribed, leads to the assumption that some of the commensal **Neisseria** species may have the potential for the expression of a protein harboring similar functions as the Opa proteins in pathogenic Neisseriae.
Tags: Comparative Study
Descriptors: Antigens, Bacterial--genetics--GE; *Bacterial Outer Membrane Proteins--genetics--GE; *Genome, Bacterial; * **Neisseria** --genetics--GE; * **Neisseria** --pathogenicity--PY; Amino Acid Sequence; Base Sequence; Chromosomes, Bacterial; DNA Primers; DNA, Bacterial--genetics--GE; Fimbriae Proteins; Molecular Sequence Data; **Neisseria** gonorrhoeae--genetics--GE; **Neisseria** gonorrhoeae--pathogenicity--PY; **Neisseria** meningitidis --genetics--GE; **Neisseria** meningitidis--pathogenicity--PY; Oligonucleotide Probes; Sequence Homology, Amino Acid; **Serine Endopeptidases --genetics** --GE; Species Specificity; Virulence--genetics--GE
Molecular Sequence Databank No.: GENBANK/U12287; GENBANK/U12288
CAS Registry No.: 0 (Antigens, Bacterial); 0 (Bacterial Outer Membrane Proteins); 0 (DNA Primers); 0 (DNA, Bacterial); 0 (Oligonucleotide Probes); 0 (gonococcal protein III); 0 (opacity protein (Neisseria gonorrhoeae)); 147680-16-8 (Fimbriae Proteins)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19950404
Record Date Completed: 19950404

9/9/21
DIALOG(R)File 155:MEDLINE(R)

08475129 95163345 PMID: 7859510
Biology of the pathogenic Neisseriae.
Meyer T F; Pohlner J; van Putten J P
Max-Planck-Institut fur Biologie, Abt. Infektionsbiologie, Tubingen, Germany.
Current topics in microbiology and immunology (GERMANY) 1994, 192 p283-317, ISSN 0070-217X Journal Code: 0110513
Document type: Journal Article; Review; Review, Academic
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
(216 Refs.)
Tags: Support, Non-U.S. Gov't
Descriptors: **Neisseria** --pathogenicity--PY; Lipopolysaccharides --toxicity--TO; Mucous Membrane--microbiology--MI; **Neisseria** --genetics --GE; **Neisseriaceae** Infections--etiology--ET; Phagocytes--immunology--IM; **Serine Endopeptidases --physiology** --PH; Transformation, Bacterial; Variation (Genetics); Virulence
CAS Registry No.: 0 (Lipopolysaccharides)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19950323
Record Date Completed: 19950323

9/9/22
DIALOG(R)File 155:MEDLINE(R)

07684511 93139760 PMID: 1487730
Identification of an outer-membrane haemoglobin-binding protein in Neisseria **meningitidis.**
Lee B C; Hill P
Department of Microbiology and Infectious Diseases, University of Calgary, Canada.
Journal of general microbiology (ENGLAND) Dec 1992, 138 (Pt 12) p2647-56, ISSN 0022-1287 Journal Code: 0375371
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
Although **Neisseria** meningitidis can use haemoglobin as an iron source in vitro, the mechanism of haemoglobin-iron uptake is unknown. Using a biotinylated human haemoglobin probe in a solid-phase dot-binding assay, haemoglobin-binding activity was detected in total membranes derived from meningococci grown under iron-limited but not iron-sufficient conditions. In competition binding experiments, bovine and human haemoglobin could abrogate binding. In contrast, no binding inhibition was seen with ferric nitrate, protoporphyrin IX, and iron-loaded human transferrin. The ability of both haemin and catalase, a nonhaemoglobin haem-containing compound, to inhibit binding competitively suggested that the ligand recognized by the binding protein is the haem moiety. Scatchard plot analysis revealed a heterogeneous receptor population. Limited proteolysis with proteinase K abolished binding activity, suggesting a haemoglobin-protein interaction. Detection of activity in a whole-cell binding assay demonstrated that this haemin-binding protein was surface exposed. In a limited survey of meningococcal strains, the presence of haemoglobin-binding activity in all isolates indicated that expression of this binding protein is not serogroup specific.

Tags: Support, Non-U.S. Gov't
Descriptors: Bacterial Outer Membrane Proteins --isolation and purification--IP; *Carrier Proteins--isolation and purification--IP; *Hemoglobins--metabolism--ME; *Iron--metabolism--ME; * **Neisseria** meningitidis--metabolism--ME; Bacterial Outer Membrane Proteins--analysis --AN; Bacterial Outer Membrane Proteins--metabolism--ME; Biological Transport; Biotin; Carrier Proteins--analysis--AN; Carrier Proteins --metabolism--ME; Endopeptidase K; Iron--pharmacology--PD; Molecular Probes ; **Neisseria** meningitidis--growth and development--GD; Receptors, Transferrin--biosynthesis--BI; **Serine Endopeptidases --pharmacology** --PD; Subcellular Fractions--chemistry--CH; Variation (Genetics)
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Carrier Proteins); 0 (Hemoglobins); 0 (Molecular Probes); 0 (Receptors, Transferrin); 0 (hemoglobin-binding protein); 58-85-5 (Biotin); 7439-89-6 (Iron)
Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.64 (Endopeptidase K)
Record Date Created: 19930225
Record Date Completed: 19930225

9/9/23
DIALOG(R)File 155:MEDLINE(R)

07599293 93054350 PMID: 1429457
Kinetics and sequence specificity of processing of prepilin by PilD, the type IV leader peptidase of Pseudomonas aeruginosa.
Strom M S; Lory S
Department of Microbiology, School of Medicine, University of Washington, Seattle 98195.
Journal of bacteriology (UNITED STATES) Nov 1992, 174 (22) p7345-51, ISSN 0021-9193 Journal Code: 2985120R
Contract/Grant No.: AI21451; AI; NIAID
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
PilD, originally isolated as an essential component for the biogenesis of the type IV pili of Pseudomonas aeruginosa, is a unique endopeptidase responsible for processing the precursors of the P. aeruginosa pilin subunits. It is also required for the cleavage of the leader peptides from the Pdd proteins, which are essential components of an extracellular secretion pathway specific for the export of a number of P. aeruginosa hydrolytic enzymes and toxins. Substrates for PilD are initially synthesized with short, i.e., 6- to 8-amino-acid-long, leader peptides with a net basic charge and share a high degree of amino acid homology through the first 16 to 30 residues at the amino terminus. In addition, they all have a phenylalanine residue at the +1 site relative to the cleavage site, which is N methylated prior to assembly into the oligomeric structures. In this study, the kinetics of leader peptide cleavage from the precursor of the P. aeruginosa pilin subunit by PilD was determined in vitro. The rates of cleavage were compared for purified enzyme and substrate as well as for enzyme and substrate contained within total membranes extracted from P. aeruginosa strains overexpressing the cloned pilD or pilA genes. Optimal conditions were obtained only when both PilD and substrate were contained within total membranes. PilD catalysis of P. aeruginosa prepilin followed normal Michaelis-Menten kinetics, with a measured apparent Km of approximately 650 microM, and a kcat of 180 min-1. The kinetics of PilD processing of another type IV pilin precursor, that from **Neisseria** gonorrhoeae with a 7-amino-acid-long leader peptide, were essentially the same as that measured for wild-type P. aeruginosa prepilin. Quite different results were obtained for a number of prepilin substrates containing substitutions at the conserved phenylalanine at the +1 position relative to the cleavage site, which were previously shown to be well tolerated in vivo. Substitutions of methionine, serine, and cysteine for phenylalanine show that Km values remain close to that measured for wild-type substrate, while kcat and kcat/Km values were significantly decreased. This indicates

that while the affinity of enzyme for substrate is relatively unaffected by the substitutions, the maximum rate of catalysis favors a phenylalanine at this position.(ABSTRACT TRUNCATED AT 400 WORDS)

Tags: Comparative Study; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Outer Membrane Proteins--genetics--GE; *Bacterial Outer Membrane Proteins--metabolism--ME; *Bacterial Proteins--metabolism --ME; * **Endopeptidases** --metabolism--ME; *Protein Precursors--metabolism --ME; *Protein Sorting Signals--genetics--GE; *Protein Sorting Signals --metabolism--ME; *Pseudomonas aeruginosa--genetics--GE; *Pseudomonas aeruginosa--metabolism--ME; Amino Acid Sequence; Escherichia coli--genetics --GE; Fimbriae Proteins; Genotype; Kinetics; Molecular Sequence Data; Phenotype; Plasmids; Sequence Homology, Amino Acid; Substrate Specificity

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (PilD protein); 0 (Plasmids); 0 (Protein Precursors); 0 (Protein Sorting Signals); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.4.- (**Endopeptidases**); EC 3.4.21.89 (signal peptidase I)

Record Date Created: 19921216

Record Date Completed: 19921216

9/9/24

DIALOG(R)File 155:MEDLINE(R)

07511134 92374839 PMID: 1354833

PulO, a component of the pullulanase secretion pathway of Klebsiella oxytoca, correctly and efficiently processes gonococcal type IV prepilin in Escherichia coli.

Dupuy B; Taha M K; Possot O; Marchal C; Pugsley A P

Unite des Neisseria, Institut Pasteur, Paris, France.

Molecular microbiology (ENGLAND) Jul 1992, 6 (14) p1887-94, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The PulO protein required for extracellular secretion of pullulanase by Klebsiella oxytoca is known to be highly homologous to two type IV prepilin peptidases, namely XcpA(PilD) (Pseudomonas aeruginosa) and TcpJ (Vibrio cholerae). The predicted prepilin peptidase activity of PulO was confirmed by showing that it could correctly process the product of the cloned pilE.1 type IV pilin structural gene from **Neisseria** gonorrhoeae in Escherichia coli. The P. aeruginosa prepilin peptidase and another putative prepilin peptidase, ComC from Bacillus subtilis, also processed prePilE. Subcellular fractionation showed that the pilE gene product that had been processed by PulO remained associated with the cytoplasmic membrane, as did the unprocessed precursor. PulO was also shown to process three of the four prePilE-PhoA hybrids tested. Southern hybridization experiments suggest that a pulO homologue is present in the N. gonorrhoeae chromosome.

Tags: Support, Non-U.S. Gov't

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; * **Endopeptidases** --metabolism--ME; *Escherichia coli--genetics--GE; *Fimbriae, Bacterial--metabolism--ME; *Genes, Bacterial--physiology--PH; *Protein Precursors--metabolism--ME; *Protein Processing, Post-Translationa l--genetics--GE; Bacterial Outer Membrane Proteins--genetics--GE; **Endopeptidases** --genetics--GE; Escherichia coli--chemistry--CH; Fimbriae Proteins; Fimbriae, Bacterial--enzymology--EN; Glycoside Hydrolases --secretion--SE; Kinetics; Klebsiella--genetics--GE; Models, Biological; **Neisseria** gonorrhoeae--genetics--GE; Nucleic Acid Hybridization; Protein Precursors--genetics--GE; Recombinant Proteins--metabolism--ME

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Protein Precursors); 0 (Recombinant Proteins); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.2.1. (Glycoside Hydrolases); EC 3.2.1.41 (pullulanase); EC 3.4.- (**Endopeptidases**); EC 3.4.99.- (type IV prepilin peptidase)

Gene Symbol: comC; pilE; pulO

Record Date Created: 19920922

Record Date Completed: 19920922

9/9/25
DIALOG(R)File 155:MEDLINE(R)

07426279 92289698 PMID: 1600950
Selective extracellular release of cholera toxin B subunit by Escherichia coli: dissection of Neisseria **Iga beta-mediated outer membrane transport.**
Klauser T; Pohlner J; Meyer T F
Max-Planck-Institut fur Biologie, Abteilung Infektionsbiologie, Tubingen, FRG.
EMBO journal (ENGLAND) Jun 1992, 11 (6) p2327-35, ISSN 0261-4189 Journal Code: 8208664
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The C-terminal domain (Iga beta) of the **Neisseria** IgA protease precursor is involved in the transport of covalently attached proteins across the outer membrane of Gram-negative bacteria. We investigated outer membrane transport in Escherichia coli using fusion proteins consisting of an N-terminal signal sequence for inner membrane transport, the Vibrio cholerae toxin B subunit (CtxB) as a passenger and Iga beta. The process probably involves two distinct steps: (i) integration of Iga beta into the outer membrane and (ii) translocation of the passenger across the membrane. The outer membrane integrated part of Iga beta is the C-terminal 30 kDa core, which serves as a translocator for both the passenger and the linking region situated between the passenger and Iga beta core. The completeness of the translocation is demonstrated by the extracellular release of the passenger protein owing to the action of the E. coli outer membrane OmpT protease. Translocation of the CtxB moiety occurs efficiently under conditions preventing intramolecular disulphide bond formation. In contrast, if disulphide bond formation in the periplasm proceeds, then translocation halts after the export of the linking region. In this situation transmembrane intermediates are generated which give rise to characteristic fragments resulting from rapid proteolytic degradation of the periplasmically trapped portion. Based on the identification of translocation intermediates we propose that the polypeptide chain of the passenger passes in a linear fashion across the bacterial outer membrane.
Tags: Support, Non-U.S. Gov't
Descriptors: Cholera Toxin--metabolism--ME; *Enzyme Precursors --metabolism--ME; *Escherichia coli--genetics--GE; * **Neisseria** --genetics --GE; * **Neisseria** --metabolism--ME; *Peptide Hydrolases--metabolism--ME; *Protein Processing, Post-Translational; * **Serine Endopeptidases --metabolism** --ME; Base Sequence; Cell Membrane--metabolism--ME; Cholera Toxin--genetics--GE; Cloning, Molecular; Enterotoxins--genetics--GE; Enterotoxins--metabolism--ME; Enzyme-Linked Immunosorbent Assay; Escherichia coli--metabolism--ME; Immunoblotting; Macromolecular Systems; Molecular Sequence Data; Oligodeoxyribonucleotides; Peptide Hydrolases --genetics--GE; Protein Conformation; Protein Sorting Signals--metabolism --ME; Recombinant Fusion Proteins--metabolism--ME; Vibrio cholerae --genetics--GE
CAS Registry No.: 0 (Enterotoxins); 0 (Enzyme Precursors); 0 (Macromolecular Systems); 0 (Oligodeoxyribonucleotides); 0 (Protein Sorting Signals); 0 (Recombinant Fusion Proteins); 0 (non-agglutinable Vibrio ST enterotoxin); 9012-63-9 (Cholera Toxin)
Enzyme No.: EC 3.4 (Peptide Hydrolases); EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase); EC 3.4.21.87 (omptin)
Record Date Created: 19920714
Record Date Completed: 19920714

9/9/26
DIALOG(R)File 155:MEDLINE(R)

06954856 91195334 PMID: 1901657

Product of the Pseudomonas aeruginosa gene pilD is a prepilin leader peptidase.

Nunn D N; Lory S

Department of Microbiology, School of Medicine, University of Washington, Seattle 98195.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Apr 15 1991, 88 (8) p3281-5, ISSN 0027-8424 Journal Code: 7505876

Contract/Grant No.: AI21451; AI; NIAID

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

The related type IV pilins produced by Pseudomonas aeruginosa, **Neisseria** gonorrhoeae, Bacteroides nodosus, and Moraxella bovis are synthesized as precursors with short, six- or seven-amino acid N-terminal leader peptides. We have previously observed that P. aeruginosa mutations in pilD, a gene required for pilus biogenesis, result in the accumulation of unprocessed prepilin in the membrane and a general defect in the excretion of a number of extracellular enzymes. An endopeptidase activity has been detected in detergent-solubilized inner membrane of P. aeruginosa and shown to correctly cleave the prepilin of P. aeruginosa and N. gonorrhoeae. It is absent from pilD mutants, increased by pilD overexpression, and conferred on Escherichia coli by the introduction of the pilD gene. The pilD gene product, purified by immunoaffinity chromatography with antibody to a PilD-derived synthetic peptide, was identified with the endopeptidase. PilD appears to be a prototype of a class of enzymes that process not only type IV pilin precursors but also components of a protein-excretion apparatus of Gram-negative bacteria.

Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Bacterial Outer Membrane Proteins--metabolism--ME; *Bacterial Proteins--metabolism--ME; * **Endopeptidases** --metabolism--ME; *Protein Precursors--metabolism--ME; *Pseudomonas aeruginosa--enzymology --EN; Amino Acid Sequence; Bacterial Proteins--chemistry--CH; Bacterial Proteins--isolation and purification--IP; Cell Membrane--enzymology--EN; Cloning, Molecular; Fimbriae Proteins; Molecular Sequence Data; Molecular Weight; Morphogenesis; Protein Processing, Post-Translational; Pseudomonas aeruginosa--genetics--GE

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Bacterial Proteins); 0 (PilD protein); 0 (Protein Precursors); 147680-16-8 (Fimbriae Proteins)

Enzyme No.: EC 3.4.- (**Endopeptidases**); EC 3.4.21.89 (signal peptidase I)

Record Date Created: 19910515

Record Date Completed: 19910515

9/9/27

DIALOG(R)File 155:MEDLINE(R)

06711946 90337964 PMID: 2116408

Identification of the primary antimicrobial domains in human neutrophil cathepsin G.

Bangalore N; Travis J; Onunka V C; Pohl J; Shafer W M

Department of Biochemistry, University of Georgia, Athens 30602.

Journal of biological chemistry (UNITED STATES) Aug 15 1990, 265 (23) p13584-8, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: AI-21150; AI; NIAID; HL-26887; HL; NHLBI

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Lysosomal cathepsin G from human neutrophils is a chymotrypsin-like protease which also possesses antimicrobial activity. The antimicrobial

activity, however, is independent of protease activity, because treatment of this enzyme with the irreversible serine protease inhibitor diisopropylfluorophosphate has no effect on its antimicrobial action. In this study, we found that digestion of cathepsin G with clostripain caused a loss of proteolytic activity in this neutrophil proteinase. However, bactericidal activity in in vitro assays against Staphylococcus aureus and **Neisseria** gonorrhoeae was retained. Fractionation of the clostripain-digested cathepsin G mixture yielded two distinct antimicrobial peptides. The sequences of these peptides were IIGGR and HPQYNQR (residues 1-5 and 77-83 in cathepsin G, respectively). Synthetic peptides corresponding to these sequences were also prepared and found to exert broad-spectrum antimicrobial activity in vitro, displaying conditions of temperature- and pH-dependent optima for antimicrobial action resembling that of the full-length enzyme. Depending on the target bacterial strain, these peptides exhibited antimicrobial activity between 5.0 x 10(-5) and 4.0 x 10(-4) M. Significantly, replacement of certain residues within these peptides with either alanine or valine significantly reduced their antibacterial capacities. Our studies suggest that cathepsin G has two antimicrobial sequences, either or both of which may contribute to its bactericidal activity.

Tags: Human; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Descriptors: *Anti-Infective Agents; *Cathepsins--blood--BL; *Neutrophils --enzymology--EN; *Oligopeptides--pharmacology--PD; Amino Acid Sequence; Cathepsins--pharmacology--PD; Cysteine **Endopeptidases** --metabolism--ME; Cysteine **Endopeptidases** --pharmacology--PD; Kinetics; Lysosomes --enzymology--EN; Molecular Sequence Data; **Neisseria** gonorrhoeae--drug effects--DE; Oligopeptides--chemical synthesis--CS; Pancreatic Elastase --blood--BL; Peptide Fragments--pharmacology--PD; Staphylococcus aureus --drug effects--DE

CAS Registry No.: 0 (Anti-Infective Agents); 0 (Oligopeptides); 0 (Peptide Fragments)

Enzyme No.: EC 3.4.- (Cathepsins); EC 3.4.21.20 (cathepsin G); EC 3.4.21.36 (Pancreatic Elastase); EC 3.4.22 (Cysteine **Endopeptidases**); EC 3.4.22.8 (clostripain)

Record Date Created: 19900913

Record Date Completed: 19900913

9/9/28

DIALOG(R)File 155:MEDLINE(R)

05545664 87224739 PMID: 3295108

Lipopolysaccharide induces recurrence of arthritis in rat joints previously injured by peptidoglycan-polysaccharide.

Stimpson S A; Esser R E; Carter P B; Sartor R B; Cromartie W J; Schwab J H

Journal of experimental medicine (UNITED STATES) Jun 1 1987, 165 (6) p1688-702, ISSN 0022-1007 Journal Code: 2985109R

Contract/Grant No.: AM-25733; AM; NIADDK; AM-30701; AM; NIADDK; AM-32137; AM; NIADDK

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Rat ankle joints injected intraarticularly with 5 micrograms of group A streptococcal peptidoglycan-polysaccharide (PG-APS) developed an acute course of arthritis. Recurrence of arthritis was induced in 100% of these joints by intravenous injection of as little as 10 micrograms of Salmonella typhimurium lipopolysaccharide (LPS) 3 wk after intraarticular injection. This reaction was similar in athymic and euthymic rats. Buffalo rats were less susceptible than Lewis or Sprague-Dawley rats. **Neisseria** gonorrhoeae, Yersinia enterocolitica, and Escherichia coli LPS, and S. typhimurium Re mutant LPS, were also active. Re mutant LPS activity was greatly reduced by mixing with polymyxin B. E. coli lipid A was weakly active. An acute synovitis of much less incidence, severity, and duration was seen in contralateral joints injected initially with saline, and in ankle joints of naive, previously uninjected rats after intravenous LPS

injection. The intravenous injection of the muramidase mutanolysin on day 0 or 7 after intraarticular PG-APS injection prevented LPS-induced recurrence of arthritis. These studies suggest that the phlogistic activities of lipid A and peptidoglycan might interact in an inflammatory disease process, and that LPS may play a role in recurrent episodes of rheumatoid arthritis or reactive arthritis.

Tags: Animal; Female; Support, U.S. Gov't, P.H.S.

Descriptors: *Arthritis--chemically induced--CI; *Lipopolysaccharides --toxicity--TO; *Peptidoglycan--toxicity--TO; *Polysaccharides, Bacterial --toxicity--TO; **Endopeptidases** --pharmacology--PD; Lipid A--toxicity--TO; Rats; Rats, Inbred BUF; Rats, Inbred Lew; Recurrence; Species Specificity; Synovitis--chemically induced--CI; T-Lymphocytes--physiology--PH

CAS Registry No.: 0 (Lipid A); 0 (Lipopolysaccharides); 0 (Peptidoglycan); 0 (Polysaccharides, Bacterial); 0 (streptococcal polysaccharide group A)

Enzyme No.: EC 3.4.- (**Endopeptidases**); EC 3.4.99.- (mutanolysin)

Record Date Created: 19870706

Record Date Completed: 19870706

9/9/29

DIALOG(R)File 155:MEDLINE(R)

05229090 86230158 PMID: 3086672

Proteases of the pathogenic neisseriae: possible role in infection.

O'Reilly T M; Bhatti A R

Microbios (ENGLAND) 1986, 45 (183) p113-29, ISSN 0026-2633 Journal Code: 0207257

Document type: Journal Article; Review

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Proteolytic enzymes are produced by animal as well as human pathogens. Several micro-organisms including Neisseriae produce IgA1 specific proteases. This protease specifically hydrolyses IgA1 protein. IgA1-specific protease(s) synthesized by **Neisseria** species are briefly reviewed with particular reference to their role in infection. (99 Refs.)

Tags: Female; Human; Male

Descriptors: **Neisseria** gonorrhoeae--enzymology--EN; * **Neisseria** meningitidis--enzymology--EN; *Peptide Hydrolases--metabolism--ME; Aminopeptidases--metabolism--ME; Asparaginase--metabolism--ME; Edetic Acid --pharmacology--PD; **Endopeptidases** --metabolism--ME; Gonorrhea--enzymology --EN; Gonorrhea--microbiology--MI; Immunoglobulin A--immunology--IM; Immunoglobulin A--metabolism--ME; Immunoglobulin A, Secretory--immunology --IM; Immunoglobulin A, Secretory--metabolism--ME; Meningitis, Meningococcal--enzymology--EN; Meningitis, Meningococcal--microbiology--MI ; Meningococcal Infections--enzymology--EN; Meningococcal Infections --microbiology--MI; Substrate Specificity

CAS Registry No.: 0 (Immunoglobulin A); 0 (Immunoglobulin A, Secretory); 60-00-4 (Edetic Acid)

Enzyme No.: EC 3.4 (Peptide Hydrolases); EC 3.4.- (**Endopeptidases**); EC 3.4.11 (Aminopeptidases); EC 3.4.21.72 (IgA-specific serine endopeptidase); EC 3.5.1.1 (Asparaginase)

Record Date Created: 19860717

Record Date Completed: 19860717

9/9/30

DIALOG(R)File 155:MEDLINE(R)

04567957 84211127 PMID: 6427111

Proteins IA and IB exhibit different surface exposures and orientations in the outer membranes of Neisseria **gonorrhoeae.**

Barrera O; Swanson J

Infection and immunity (UNITED STATES) Jun 1984, 44 (3) p565-8, ISSN 0019-9567 Journal Code: 0246127

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

Exposure of whole gonococci to proteinase K resulted in cleavage of protein I (P.I) of the organism in situ. P.I subunits in the P.IB group were cleaved into two membrane-associated fragments, whereas P.IA subunits were cleaved by proteinase K to yield a single membrane-associated fragment slightly smaller in apparent size than the intact P.IA subunit. These data suggest that P.IA and P.IB subunits are quite different in their surface exposures and orientations in the gonococcal outer membrane; P.IB subunits likely have both termini buried in the membrane, whereas P.IA subunits have one of their termini exposed on the surface of the organism.

Descriptors: Membrane Proteins--analysis--AN; * **Neisseria** gonorrhoeae --analysis--AN; Bacterial Outer Membrane Proteins; Cell Membrane--analysis --AN; Chymotrypsin--metabolism--ME; Electrophoresis, Polyacrylamide Gel; Endopeptidase K; **Endopeptidases** --metabolism--ME; Macromolecular Systems; Molecular Weight; Peptide Fragments--analysis--AN

CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (Macromolecular Systems); 0 (Membrane Proteins); 0 (Peptide Fragments)

Enzyme No.: EC 3.4.- (**Endopeptidases**); EC 3.4.21.1 (Chymotrypsin); EC 3.4.21.64 (Endopeptidase K)

Record Date Created: 19840717
Record Date Completed: 19840717

9/9/31

DIALOG(R)File 155:MEDLINE(R)

04137498 83267449 PMID: 6409989

Peptidoglycan-degrading enzymes in ether-treated cells of Neisseria **gonorrhoeae.**

Chapman S J; Perkins H R

Journal of general microbiology (ENGLAND) Mar 1983, 129 (Pt 3) p877-83, ISSN 0022-1287 Journal Code: 0375371

Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS

The incubation of peptidoglycan fragments with ether-treated cells of **Neisseria** gonorrhoeae resulted in breakdown products that showed the presence of previously undescribed lytic enzymes. The properties of an endopeptidase able to hydrolyse peptide-linked bis-disaccharide peptide dimer to monomer units were examined. An exo-N-acetyl-glucosaminidase was also shown to release free N-acetylglucosamine. The breakdown pattern of glycosidically-linked dimer indicated the existence of an endo-N-acetylglucosaminidase. The activities of the latter enzyme and of the endopeptidase were both sensitive to beta-lactam antibiotics.

Tags: Support, Non-U.S. Gov't

Descriptors: Ether, Ethyl--pharmacology--PD; *Ethyl Ethers--pharmacology --PD; * **Neisseria** gonorrhoeae--enzymology--EN; *Peptidoglycan--metabolism --ME; Acetylglucosaminidase--metabolism--ME; Antibiotics, Lactam --pharmacology--PD; **Endopeptidases** --metabolism--ME; Hydrogen-Ion Concentration; **Neisseria** gonorrhoeae--drug effects--DE; Temperature

CAS Registry No.: 0 (Antibiotics, Lactam); 0 (Ethyl Ethers); 0 (Peptidoglycan); 60-29-7 (Ether, Ethyl)

Enzyme No.: EC 3.2.1.30 (Acetylglucosaminidase); EC 3.4.- (**Endopeptidases**)

Record Date Created: 19830923
Record Date Completed: 19830923

9/9/32

DIALOG(R)File 155:MEDLINE(R)

03606204 82016735 PMID: 6792682
Secretory immunity and the bacterial IgA proteases.
Kornfeld S J; Plaut A G
Reviews of infectious diseases (UNITED STATES) May-Jun 1981, 3 (3) p521-34, ISSN 0162-0886 Journal Code: 7905878
Contract/Grant No.: AI-14648; AI; NIAID; AM-07024; AM; NIADDK; AM-17194; AM; NIADDK
Document type: Journal Article; Review
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: INDEX MEDICUS
The characteristics and functions of microbial IgA proteases are reviewed. These enzymes represent a structurally heterogeneous group of proteins that are secreted into the extracellular environment by bacteria capable of causing human disease. The IgA proteases, which vary in their requirements for metal ions, are neutral **endopeptidases** whose role in the infectious process is not known but whose pronounced substrate specificity for human proteins of the IgA1 subclass has repeatedly been demonstrated. As reagents, the IgA proteases are useful in cleaving IgA molecules to yield intact Fc alpha and Fab alpha fragments that will allow the study of the structure and function of the two large regions of IgA immunoglobulin proteins. The role, if any, of these enzymes in promoting infection by pathogenic members of the genera **Neisseria** , Hemophilus, and Streptococcus is not known, although the secretory immune system is primarily mediated by antibodies of the IgA isotype, among which are IgA1 subclass proteins, and these proteins are susceptible to cleavage by IgA protease. The determination of the role of these enzymes in the pathogenesis of human infection must await clearer understanding of antigenicity and antibody function at secretory sites and of the relative roles of the two subclasses of human IgA in immune defense. (57 Refs.)
Tags: Human; Support, U.S. Gov't, P.H.S.
Descriptors: *Bacteria--enzymology--EN; *Immunoglobulin A; *Immunoglobulin A, Secretory; *Peptide Hydrolases--metabolism--ME; Immunoglobulin A--immunology--IM; Immunoglobulin A--metabolism--ME; Immunoglobulin A--secretion--SE; Immunoglobulin A, Secretory--immunology--IM; Immunoglobulins, Fab--metabolism--ME; Immunoglobulins, Fc--metabolism--ME; Models, Biological; **Neisseria** gonorrhoeae--enzymology--EN; **Neisseria** meningitidis--enzymology--EN; Peptide Hydrolases--secretion--SE; Streptococcus sanguis--enzymology--EN; Substrate Specificity
CAS Registry No.: 0 (Immunoglobulin A); 0 (Immunoglobulin A, Secretory); 0 (Immunoglobulins, Fab); 0 (Immunoglobulins, Fc)
Enzyme No.: EC 3.4 (Peptide Hydrolases); EC 3.4.21.72 (IgA-specific serine endopeptidase)
Record Date Created: 19811118
Record Date Completed: 19811118

9/9/33
DIALOG(R)File 155:MEDLINE(R)

02938689 79114384 PMID: 763311
IgA protlease.
Sullivan B J
New England journal of medicine (UNITED STATES) Mar 29 1979, 300 (13) p737, ISSN 0028-4793 Journal Code: 0255562
Document type: Letter
Languages: ENGLISH
Main Citation Owner: NLM
Record type: Completed
Subfile: AIM; INDEX MEDICUS
Descriptors: **Endopeptidases** --metabolism--ME; *Immunoglobulin A --metabolism--ME; * **Neisseriaceae** --enzymology--EN
CAS Registry No.: 0 (Immunoglobulin A)
Enzyme No.: EC 3.4.- (**Endopeptidases**)
Record Date Created: 19790428
Record Date Completed: 19790428
?logoff hold

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     $0.92  TELNET
    $16.70  Estimated cost this search
    $16.70  Estimated total session cost   2.923 DialUnits


### Status: Signed Off. (4 minutes)
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cleave serum IgAs of gorillas, chimpanzees, and orangutans. All enzymes cleaved the IgAs of the three apes despite differences in ape IgA1 hinge sequence relative to the human prototype. To directly compare the ape and human hinge cleavage sites, the sites were identified in eight ape IgA digests. This analysis confirmed that ape proteins were all cleaved in the IgA hinge region, in all but one case after proline residues. The exception, C. ramosum protease, cleaved gorilla and chimpanzee IgAs at peptide bonds having no proline, but the scissile bonds were in the same hinge location as the Pro-221-Val-222 cleaved in human IgA1. These data indicate that proline is not an invariant substrate requirement for all IgA proteases and that the location of the scissile bond, in addition to its composition, is a critical determinant of cleavage specificity.

Tags: Animal; Comparative Study; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Bacteria--enzymology--EN; *Immunoglobulin A--metabolism--ME; * **Serine Endopeptidases** **--metabolism** --ME; Amino Acid Sequence; Gorilla gorilla; Immunoglobulin A--chemistry--CH; Molecular Sequence Data; Pan troglodytes; Pongo pygmaeus; Substrate Specificity

CAS Registry No.: 0 (Immunoglobulin A)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19960716

Record Date Completed: 19960716

9/9/10

DIALOG(R)File 155:MEDLINE(R)

10346713 96149195 PMID: 8544214

Lack of interference between IgA-binding proteins and IgA proteases of human pathogenic bacteria.

Stenberg L; Qiu J; Lindahl G; Plaut A G

Department of Medical Microbiology, Lund University, Sweden.

Journal of medical microbiology (SCOTLAND) Jan 1996, 44 (1) p65-9, ISSN 0022-2615 Journal Code: 0224131

Contract/Grant No.: DE 09677; DE; NIDCR; DK-34928; DK; NIDDK

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Some human bacterial pathogens produce specific immunoglobulin A1 (IgA1) proteases that cleave the heavy chain of human IgA1, generating intact Fab and Fc fragments. Other pathogenic bacterial species express surface proteins which bind to the Fc part of human IgA in a non-immune manner. To analyse whether IgA-binding proteins affect the activity of IgA1 proteases, the ability of seven different IgA1 proteases to hydrolyse IgA1 in the presence of either of two different bacterial IgA-binding proteins was tested. Data obtained in two different types of experiment suggest that IgA1 bound to IgA-binding proteins still functions as a substrate for IgA1 proteases. As Fc fragments produced by cleaving IgA1 with IgA1 proteases still bind to IgA-binding proteins, we conclude that these two types of bacterial protein act independently of each other.

Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: Haemophilus influenzae--immunology--IM; *Lymphokines --metabolism--ME; * **Neisseria** --immunology--IM; * **Serine Endopeptidases** **--metabolism** --ME; *Streptococcus--immunology--IM; Autoradiography; Electrophoresis, Polyacrylamide Gel; Haemophilus influenzae--enzymology--EN ; **Neisseria** --enzymology--EN; Streptococcus--enzymology--EN

CAS Registry No.: 0 (Lymphokines); 0 (immunoglobulin-binding factors)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19960214

Record Date Completed: 19960214

9/9/11

DIALOG(R)File 155:MEDLINE(R)

10328569 96130840 PMID: 8594327

Uptake and nuclear transport of Neisseria **IgA1 protease-associated alpha-proteins in human cells.**

Pohlner J; Langenberg U; Wolk U; Beck S C; Meyer T F

Max-Planck-Institut fur Biologie, Abteilung, Infektionsbiologie, Tubingen, Germany.

Molecular microbiology (ENGLAND) Sep 1995, 17 (6) p1073-83, ISSN 0950-382X Journal Code: 8712028

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: INDEX MEDICUS

Pathogenic **Neisseria** species, the causative agents of gonorrhoea and bacterial meningitis, encode a family of polymorphic exo-proteins which are autoproteolytically processed into several distinct extracellular components, including an IgA1 protease and an alpha-protein. IgA1 protease, a putative virulence determinant, is a sequence-specific endopeptidase known to cleave human IgA1, but additional target proteins have been postulated. The physical linkage of IgA1 protease and alpha-protein suggests a functional relationship of both precursor components. Previous work has shown that alpha-protein is essential neither for extracellular transport nor for the proteolytic activity of IgA1 protease. Intriguingly, alpha-proteins carry amino acid sequences reminiscent of nuclear location signals of viral and eukaryotic proteins. Here we demonstrate the functionality of these nuclear location signal sequences in transfected eukaryotic cells. Chimeric alpha-proteins show nuclear transport and selectively associate with nucleolar structures. More importantly, native purified alpha-proteins are capable of entering certain human primary cells from the exterior via an endocytotic route and accumulate in the nuclei. The neisserial alpha-proteins share several features with eukaryotic transcription factors, such as the formation of dimers via a heptad repeat sequence. We propose a role for alpha-proteins in the regulation of host-cell functions. As the alpha-proteins are covalently connected with IgA1 protease they may also serve as carries for the IgA1 protease into human cells where additional proteolytic targets may exist. **Neisseria** meningitidis, which locally colonizes the nasopharyngeal mucosa of many human individuals without apparently causing symptoms, secretes this nucleus-targeted factor in large quantities.

Tags: Comparative Study; Human; Support, Non-U.S. Gov't

Descriptors: Bacterial Proteins--metabolism--ME; * **Neisseria** gonorrhoeae --metabolism--ME; * **Neisseria** meningitidis--metabolism--ME; * **Serine Endopeptidases --metabolism** --ME; Amino Acid Sequence; Bacterial Proteins --chemistry--CH; Base Sequence; Biological Transport; Cell Nucleus --metabolism--ME; Cells, Cultured; Cornea--cytology--CY; Epithelial Cells; Genes, Reporter; Models, Molecular; Molecular Sequence Data; **Neisseria** gonorrhoeae--pathogenicity--PY; **Neisseria** meningitidis--pathogenicity --PY; Protein Conformation; Protein Sorting Signals--chemistry--CH; Recombinant Fusion Proteins--metabolism--ME; Sequence Alignment; Sequence Homology, Amino Acid; **Serine Endopeptidases --chemistry** --CH; Transfection; Virulence

CAS Registry No.: 0 (Bacterial Proteins); 0 (Protein Sorting Signals) ; 0 (Recombinant Fusion Proteins)

Enzyme No.: EC 3.4.21 (Serine **Endopeptidases**); EC 3.4.21.72 (IgA-specific serine endopeptidase)

Record Date Created: 19960411

Record Date Completed: 19960411

9/9/12

10315976 96118130 PMID: 8578806

Neisseria **gonorrhoeae IgA1 proteases share epitopes recognized by neutralizing antibodies.**

Lomholt H; Lind I; Kilian M